SEQUENCE LISTING

<110> Glucksmann, Maria Alexsandra
Gimeno, Ruth
White, David

<120> 57242, a Human G-Protein Coupled Receptor Family Member and Uses Therefor

<130> MPI2000-368P1R

<150> US 60/228,409
<151> 2000-08-29

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gctctgcacc cggacacctg ctctgtcccc gcc atg tac aac ggg tcg tgc tgc  174
                                    Met Tyr Asn Gly Ser Cys Cys
                                     1               5

cgc atc gag ggg gac acc atc tcc cag gtg atg ccg ccg ctg ctc att   222
Arg Ile Glu Gly Asp Thr Ile Ser Gln Val Met Pro Pro Leu Leu Ile
         10                  15                  20

gtg gcc ttt gtg ctg ggc gca cta ggc aat ggg gtc gcc ctg tgt ggt   270
Val Ala Phe Val Leu Gly Ala Leu Gly Asn Gly Val Ala Leu Cys Gly
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ttc tgc ttc cac atg aag acc tgg aag ccc agc act gtt tac ctt ttc   318
Phe Cys Phe His Met Lys Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe
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aat ttg gcc gtg gct gat ttc ctc ctt atg atc tgc ctg cct ttt cgg   366
Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Phe Arg
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aca gac tat tac ctc aga cgt aga cac tgg gct ttt ggg gac att ccc   414
Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly Asp Ile Pro
             75                  80                  85

tgc cga gtg ggg ctc ttc acg ttg gcc atg aac agg gcc ggg agc atc   462
Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala Gly Ser Ile
         90                  95                  100

gtg ttc ctt acg gtg gtg gct gcg gac agg tat ttc aaa gtg gtc cac   510
Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys Val Val His
    105                 110                 115

ccc cac cac gcg gtg aac act atc tcc acc cgg gtg gcg gct ggc atc   558
Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala Ala Gly Ile
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gtc tgc acc ctg tgg gcc ctg gtc atc ctg gga aca gtg tat ctt ttg   606
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Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val Tyr Leu Leu
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Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser Cys Glu Ser
            155                 160                 165

ttc atc atg gag tcg gcc aat ggc tgg cac gac atc atg ttc cag ctg   702
Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln Leu
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gag ttc ttt atg ccc ctc ggc atc atc tta ttt tgc tcc ttc aag att   750
Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser Phe Lys Ile
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gtt tgg agc ctg agg cgg agg cag cag ctg gcc aga cag gct cgg atg   798
Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln Ala Arg Met
200                 205                 210                 215

aag aag gcg acc cgg ttc atc atg gtg gtg gca att gtg ttc atc aca   846
Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val Phe Ile Thr
                220                 225                 230

tgc tac ctg ccc agc gtg tct gct aga ctc tat ttc ctc tgg acg gtg   894
Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu Trp Thr Val
            235                 240                 245

ccc tcg agt gcc tgc gat ccc tct gtc cat ggg gcc ctg cac ata acc   942
Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu His Ile Thr
        250                 255                 260

ctc agc ttc acc tac atg aac agc atg ctg gat ccc ctg gtg tat tat   990
Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr
    265                 270                 275

ttt tca agc ccc tcc ttt ccc aaa ttc tac aac aag ctc aaa atc tgc   1038
Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu Lys Ile Cys
280                 285                 290                 295

agt ctg aaa ccc aag cag cca gga cac tca aaa aca caa agg ccg gaa   1086
Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln Arg Pro Glu
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gag atg cca att tcg aac ctc ggt cgc agg agt tgc atc agt gtg gca   1134
Glu Met Pro Ile Ser Asn Leu Gly Arg Arg Ser Cys Ile Ser Val Ala
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aat agt ttc caa agc cag tct gat ggg caa tgg gat ccc cac att gtt   1182
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Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
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Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
            100                 105                 110
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
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Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
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Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
145                 150                 155                 160
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
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His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
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Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
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Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
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Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
225                 230                 235                 240
Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
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His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
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Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
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Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
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Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
305                 310                 315                 320
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
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